## I. AMENDMENT

**In the Claims:**

Please replace the claims with the following listings of claims:

1. to 5. (Canceled).

6. (Currently Amended) A diagnostic system for quantitating the individual contribution of a mutation or combination of mutations to a drug resistance phenotype exhibited by an HIV strain, said system comprising:

~~means for obtaining a genetic sequence of said HIV strain;~~

~~means for identifying the mutation pattern in said genetic sequence as compared to wild type HIV; and~~

computer means for predicting the fold resistance exhibited by said HIV strain using a method comprising the steps of:

~~1)~~ performing a linear regression analysis using data from a dataset of matching genotypes and phenotypes, wherein the log fold resistance, pFR, of each said HIV strain is modeled as the sum of all ~~the~~ individual resistance contributions for each of said mutations or combinations of mutations that occur in HIV according to the following equation;

$$pFR = \beta_A M_A + \beta_B M_B + \beta_n M_n + \cdots + \beta_Z M_Z + \varepsilon$$

wherein each said individual resistance contribution is calculated by multiplying a mutation factor, $M_A$ , $M_B$ , ..., $M_Z$, for each of said mutation or combination of mutations by a resistance coefficient $\beta_A$, $\beta_B$, ..., $\beta_Z$;

wherein for a combination of mutations, said mutation factor $M_n$ represents the co-occurrence of one mutation with other one or more mutations and said coefficient $\beta_n$ represents the synergy or antagonism between said one mutation with said other one or more mutations;

wherein said mutation factor assigned to each said mutation or combination of mutations reflects the degree to which said mutation or combination of mutations is present in said HIV strain and, if present, to which degree said mutation is present in a mixture;

wherein each said resistance coefficient reflects the contribution of said mutation or combination of mutations to said fold resistance exhibited by said strain;

wherein the error term $\varepsilon$, represents the difference between a modeled prediction and an experimentally determined measurement;

~~2)~~when pFR contains a censored value, said method further comprising replacing ~~the~~ said pFR containing said censored value in said data from said dataset of matching genotype and phenotype by a maximum likelihood estimation;

wherein ~~for each iteration of said linear regression,~~ said maximum likelihood estimation is generated according to the following steps:

a) calculating a linear regression model without said censored values;

for each said pFR containing said censored value, using a phenotypic measured value $V_0$ as said pFR of said data of said dataset of matching genotypes and phenotypes ~~as if the censor was " = ", when a result is expressed as "log $FR < 4$, $V_0$ is treated as "log $FR = 4$~~;

e) ~~using the~~ a prediction P from said linear regression model, wherein ~~to apply either~~:

i) when ~~said phenotypic value is smaller than said range, a '<' censor is applied to said value~~censor of said censored value is '<':

ia) $P < V_0 - 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove $V_0$ value from a training data for ~~the next iteration~~ following step b

~~ii~~ib) $V_0 - 0.798\ \sigma \leq P < V_0$

Use V' for $V_0$ value, wherein $V' = V_0 - 0.798\ \sigma$ for ~~the next iteration~~ following step b

~~iii~~ic) $V_0 \leq P$

Use V' for $V_0$ vlaue, wherein V' is center of gravity of tail (<V) of a normal distribution N (P, σ) as value for ~~the next iteration~~ following step b

ii) when ~~said phenotypic value is higher than said range, a '>' censor is applied to said value $V_0$~~censor of said censored value is '>':

iia) $P > V_0 + 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove $V_0$ value from training data for ~~the next iteration~~ following step b

iib) $V_0 + 0.798\ \sigma \geq P > V_0$

Use V' for $V_0$ value, wherein $V' = V_0 - 0.798\ \sigma$ for ~~the next iteration~~ following step b

iic) $V_0 \geq P$

Use V' for $V_0$ value, wherein V' center of gravity of tail (>V) of a normal distribution N (P, σ) as value for ~~the next iteration~~ following step b;

b) re-calculating ~~a~~said linear regression model ~~and for said censored values in said linear regression model, either remove the data point from the training set, or use V' instead of the censored phenotype measurement, as described in step c~~);

c) reiterating steps b) to ~~d~~c) until ~~the prediction~~said model converges;

thereby quantitating the individual contribution of said mutation or combination of mutations to said drug resistance phenotype exhibited by said HIV strain.

7. to 16. (Canceled).